In the Claims

The following is a detailed listing of all claims that are, or were, pending in the present application. Please amend claims 42 and 46, add claims 50 and 51, and cancel claims 47 and 49, as set forth in this detailed listing.

23. (previously amended) The method according to claim 44, wherein said detectable label comprises a fluorophore.

24. (previously amended) The method according to claim 44, wherein said detectable label comprises biotin.

25. (previously amended) The method according to claim 44, wherein said detectable label comprises imine-biotin.

26. (currently amended) The method according to claim 42, 50, or 51, wherein said dNTP comprises a functional group for addition of a fluorophore.

29. (currently amended) The method according to claim 42, 50, or 51, wherein said substrate is a fiber optic bundle.

30. (currently amended) The method according to claim 42, 50, or 51, wherein said substrate is selected from the group consisting of glass and plastic.

31. (previously amended) The method according to claim 44, wherein said detectable label is a fluorophore.

42. (currently amended) A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing a hybridization complex comprising

i) a first target sequence comprising

1) a first nucleotide at a detection position; ~~and~~

2) a first target domain directly 5' adjacent to said detection position; and

3) a second target domain 3' adjacent to said detection position;

ii) a first ligation probe hybridized to said first target domain; and

iii) a second ligation probe hybridized to said second target domain;

b) contacting said hybridization complex with:

i) an extension enzyme;

ii) at least one dNTP;

such that if the base of said dNTP is perfectly complementary to the base of said detection position, said first ligation probe is extended to form a ligation structure;

c) contacting said ligation structure with a ligase to ligate said first extended ligation probe and said second ligation probe to form a ligation product; and

d) detecting the presence of said ligation product to identify the nucleotide at said detection position, said detecting comprising providing a substrate with a surface comprising

i) discrete sites, and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a capture probe, wherein said capture probe hybridizes to a sequence contained within said ligation product or its complement.

43. (currently amended) The method according to claim 42 or 51, wherein one of said ligation probes comprises an adapter sequence that hybridizes to said capture probe.

44. (currently amended) The method according to claim 42, 50, or 51, wherein said dNTP comprises a detectable label.

46. (currently amended) The method according to claim 42 or 51, wherein said capture probe is a nucleic acid.

47. (cancelled)

48. (currently amended) The method according to claim 42, 50, or 51, wherein said discrete sites are wells.

49. (cancelled)

50. (new) A method of determining the identification of a nucleotide at a detection position in at least a first and a second target sequence, said method comprising:

a) providing a first hybridization complex comprising:
   i) a first target sequence comprising:
      1) a first nucleotide at a first detection position;
      2) a first target domain directly 5' adjacent to said first detection position; and
      3) a second target domain 3' adjacent to said first detection position;
   ii) a first ligation probe hybridized to said first target domain; and
   iii) a second ligation probe hybridized to said second target domain;
b) providing a second hybridization complex comprising:
   i) a second target sequence comprising:
      1) a second nucleotide at a second detection position; and
      2) a third target domain directly 5' adjacent to said second detection position;
      3) a fourth target domain 3' adjacent to said second detection position;
   ii) a third ligation probe hybridized to said third target domain;

iii) a fourth ligation probe hybridized to said fourth target domain;

c) contacting said first and second hybridization complexes with:

i) an extension enzyme;

ii) at least one dNTP;

such that if the base of said at least one dNTP is perfectly complementary to the base of said first detection position, said first ligation probe is extended to form a first ligation structure; and

such that if the base of said at least one dNTP is perfectly complementary to the base of said second detection position, said third ligation probe is extended to form a second ligation structure;

d) contacting said first and second ligation structures with a ligase to form a first and a second ligation product, respectively; and

e) detecting the presence of said first and second ligation products to identify the first and second nucleotides at said first and second detection positions, said detecting comprising providing a substrate with a surface comprising:

i) discrete sites; and

ii) a population of microspheres distributed at said sites, the population comprising at least a first and a second subpopulation, the first and second subpopulations comprising a first and a second capture probe, respectively, wherein said capture probes hybridize to a first and a second sequence contained within said first and second ligation products, or their complements respectively.

51. (new) A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing a hybridization complex comprising

i) a first target sequence comprising

1) a first nucleotide at a detection position;

2) a first target domain directly 5' adjacent to said detection position; and

3) a second target domain 3' adjacent to said detection position;

ii) a first ligation probe hybridized to said first target domain; and

iii) a second ligation probe hybridized to said second target domain;

b) contacting said hybridization complex with:

i) an extension enzyme;

ii) at least one dNTP;

such that if the base of said dNTP is perfectly complementary to the base of said detection position, said first ligation probe is extended to form a ligation structure;

c) contacting said ligation structure with a ligase to ligate said first extended ligation probe and said second ligation probe to form a ligation product; and

d) detecting the presence of said ligation product to identify the nucleotide at said detection position, said detecting comprising providing a substrate with a surface comprising

i) discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, said microspheres being randomly distributed on said substrate, wherein each subpopulation comprises a capture probe, wherein said capture probe hybridizes to a sequence contained within said ligation product or its complement.

52. (new) The method according to claim 50, wherein one of said ligation probes comprises an adapter sequence that hybridizes to one of said capture probes.

53. (new) The method according to claim 50, wherein said capture probes are nucleic acids.